

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1-22. (cancelled)

23. (currently amended) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to from HIV-1_{BRU} by from 9.8 to 12% in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein,
wherein the HIV-1 variant virus binds antibodies in AIDS patient sera,
said antibodies binding specifically to the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641,
wherein the genetic structure of said HIV-1 variant is 5'-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3', and
wherein the nucleic acid of said HIV-1 variant virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe comprising~~ the genomic cDNA of HIV-1_{MAL} as shown in Figures 7A-7I over its entire length; and
said LAV_{MAL} virus contains at least one direct sequence repeat.

24. (cancelled)

25. (currently amended) The HIV-1 variant virus of claim 23, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a ~~DNA probe comprising~~ a restriction enzyme fragment of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

26-43. (cancelled)

44. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Env sequence of HIV-1_{MAL} as shown in Figure 3.

45. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Gag sequence of HIV-1_{MAL} as shown in Figure 3.

46. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Pol sequence of HIV-1_{MAL} as shown in Figure 3.

47. (cancelled)

48. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to ~~from~~ HIV-1_{BRU} ~~by from 0.8 to 12%~~ in the entire Gag protein, from

92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~
in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the
COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM)
under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5'-LTR-gag-pol-vif-vpr-tat-rev-
vpu-env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent
hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe~~
~~comprising~~ the genomic cDNA of the virus deposited at the COLLECTION
NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641
over its entire length; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the
restriction map shown in Fig. 1.

49. (previously presented) The purified human immunodeficiency virus
designated LAV_{MAL} of claim 48, wherein the genome of LAV_{MAL} has the restriction
map shown in Fig. 1.

50. (currently amended) A purified human immunodeficiency virus
designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to from HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-gag-pol-vif-vpr-tat-rev-vpu-env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe~~ ~~comprising~~ the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641 over its entire length; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 1 to 530; 34-530; and 531-877.

51. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level ~~to from~~ HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe~~ comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641 over its entire length; and

~~said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 37-130, 211-289, 488-530, 490-620, and 680-700~~ said LAV_{MAL} virus contains at least one direct sequence repeat.

52. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level ~~to from~~ HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the
COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM)
under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to ~~a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641~~ over its entire length, ~~or a restriction enzyme fragment thereof, wherein the restriction enzyme is selected from at least one of the group consisting of Aval, BamHI, BglII, EcoRI, HincII, HindIII, KpnI, NdeI, PstI, SacI, and XbaI; and~~

the genome of said LAV_{MAL} virus comprises at least one restriction site of the restriction map shown in Fig. 1.

53. (New) The purified HIV-1 variant virus of claim 23, wherein the direct repeat is perfectly conserved.

54. (New) The purified HIV-1 variant virus of claim 23, wherein the direct repeat contains one or two point mutations.

55. (New) The purified HIV-1 variant virus of claim 23, wherein the direct sequence repeats comprise at least one of QQAAAA in HIV-1_{MAL} Gag, RAEP in HIV-1_{MAL} ORF F, DAVSQ in HIV-1_{MAL} ORF F, AVNGT in HIV-1_{MAL} Env, and DNS HIV-1_{MAL} Env.

56. (New) The purified HIV-1 variant virus of claim 23, wherein the direct sequence repeats comprise all of QQAAAA in HIV-1_{MAL} Gag, RAEP in HIV-1_{MAL} ORF F, DAVSQ in HIV-1_{MAL} ORF F, AVNGT in HIV-1_{MAL} Env, and DNS HIV-1_{MAL} Env.